Marked-up specification

Starting at page 8, please delete lines 25-32 to page 9, lines 1-5, and substitute the following:

--In a particularly preferred embodiment of the invention, the new sequences SEQ ID NO. 3 or SEQ ID NO. [3a] 21 and the new sequences SEQ ID NO. 4 or SEQ ID NO. [4a] 22, or the variants thereof obtained by deletion, substitution or addition, which can be produced on a chemical-synthetic route, are used as primer P1 and as primer P2, respectively, in the inventive detection of the RRS gene which has the NA sequence SEQ ID NO. 1 and, according to experts' estimates, is contained in 20,000 - 30,000 kinds of foods. The new NA sequence SEQ ID NO. 2 or SEQ ID NO. [2a] 20 or the variants thereof obtained by deletion, substitution or addition were found to be particularly suitable as probe S1. The preparation thereof can also be performed on a chemical-synthetic route.--

At page 9, please delete lines 6-28, and substitute the following:

--The lectin gene was found to be particularly suited as reference gene in the inventive detection of the RRS gene. When using

lectin (cf., SEQ ID NO. 11) as reference gene, the sequences SEQ ID NO. 6 or SEQ ID NO. [6a] 23 and SEQ ID NO. 7 or variants thereof obtained by deletion, substitution or addition are used as primers P3 and P4 in a preferred embodiment of the invention. The new NA sequence SEQ ID NO. 5 or variants thereof obtained by deletion, substitution or addition were found to be particularly suited as probe S3. Like probe S1, the probe S3 is labelled at its 5' end or its 3' end with a reporter fluorescent dye, and with a quencher at its other end.

According to the invention, internal amplification controls are used in the transgene determination and in the reference gene determination. The NA sequences SEQ ID NO. 8 or variants thereof obtained by deletion, substitution or addition were found to be particularly suitable internal amplification controls for the transgene determination (target IAC DNA), and the NA sequence SEQ ID NO. 10 or SEQ ID NO. [10a] 25 or variants thereof obtained by deletion, substitution or addition were found to be particularly suitable internal amplification controls for the reference gene determination in the detection of the RRS gene.--

Marked up claims

3. (Amended once) The method according to claim 1, wherein the nucleic acid sequence SEQ ID NO. 2 or SEQ ID NO. [2a] 20 or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as probe S1.

4. (Amended once) The method according to claim 1, wherein the nucleic acid sequence SEQ ID NO. 3 or SEQ ID NO. [3a] 21 and the nucleic acid sequence SEQ ID NO. 4 or SEQ ID NO. [4a] 22 or the variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as primer P1 and primer P2, respectively.

7. (Amended once) The method according to claim 1, wherein the NA sequence SEQ ID NO. 6 or SEQ ID NO. [6a] 23 and the NA sequence SEQ ID NO. 7 or the variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as primer P3 and primer P4, respectively.

8. (Amended once) The method according to claim 1, wherein the NA sequence SEQ ID NO. 8 or SEQ ID NO. [8a] 24 or variants thereof obtained by deletion, substitution or addition

and having at least 80% homology are used as synthetic gene fragment of the internal amplification control for transgene determination (target IAC DNA).

9. (Amended once) The method according to claim 1, wherein the NA sequence SEQ ID NO. 10 or SEQ ID NO. [10a] 25 or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as synthetic gene fragment of the internal amplification control for reference gene determination (reference IAC DNA).